Restriction Map of the RSV G Gene
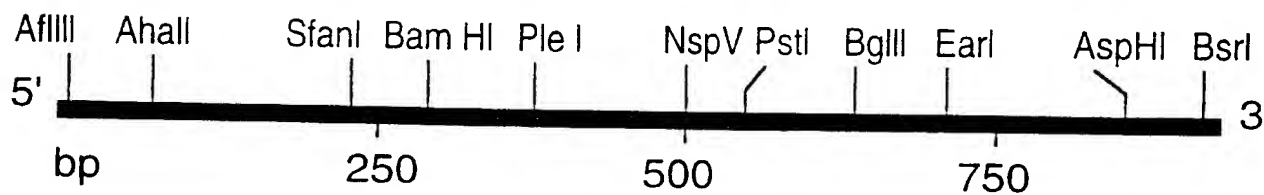

FIG.1

FIG.2A

```
      10        19        28        37        46        55
TGCAAAC ATG TCC AAA AAC AAG GAC CAA CGC ACC GCT AAG ACA CTA GAA AAG ACC
        Met Ser Lys Asn Lys Asp Gln Arg Thr Ala Lys Thr Leu Glu Lys Thr

      64        73        82        91       100       109
TGG GAC ACT CTC AAT CAT TTA TTA TTC ATA TCA TCG GGC TTA TAT AAG TTA AAT
Trp Asp Thr Leu Asn His Leu Leu Phe Ile Ser Ser Gly Leu Tyr Lys Leu Asn

     118       127       136       145       154       163
CTT AAA TCT GTA GCA CAA ATC ACA TTA TCC ATT CTG GCA ATG ATA ATC TCA ACT
Leu Lys Ser Val Ala Gln Ile Thr Leu Ser Ile Leu Ala Met Ile Ile Ser Thr

     172       181       190       199       208       217
TCA CTT ATA ATT ACA GCC ATC ATA TTC ATA GCC TCG GCA AAC CAC AAA GTC ACA
Ser Leu Ile Ile Thr Ala Ile Ile Phe Ile Ala Ser Ala Asn His Lys Val Thr

     226       235       244       253       262       271
CTA ACA ACT GCA ATC ATA CAA GAT GCA ACA AGC CAG ATC AAG AAC ACA ACC CCA
Leu Thr Thr Ala Ile Ile Gln Asp Ala Thr Ser Gln Ile Lys Asn Thr Thr Pro

     280       289       298       307       316       325
ACA TAC CTC ACT CAG GAT CCT CAG ATC CTT GGA ATC AGC TTC TCC AAT CTG TCT GAA
Thr Tyr Leu Thr Gln Asp Pro Gln Leu Gly Ile Ser Phe Ser Asn Leu Ser Glu
```

FIG.2B

```
        334         343         352         361         370         379
    ATT ACA CAA ACC ACC ATA GCT TCA ACA CCA GGA GTC AAG TCA
    Ile Thr Ser Gln Thr Thr Ile Leu Ala Ser Thr Thr Pro Gly Val Lys Ser

        388         397         406         415         424         433
    AAC CTG CAA CCC ACA GTC AAG ACT AAA AAC ACA ACA CAA CAA
    Asn Leu Gln Pro Thr Val Lys Thr Val Lys Thr Asn Thr Thr Gln Thr Gln Gln

        442         451         460         469         478         487
    CCC AGC AAG CCC ACT ACA AAA CAA CGC CAA AAC AAA CCC AAT
    Pro Ser Lys Pro Thr Lys Pro Thr Lys Gln Arg Gln Asn Lys Pro Pro Asn

        496         505         514         523         532         541
    AAT GAT TTT CAC TTC GAA GTG TTT AAC TTT GTA CCC TGC AGC AAC
    Asn Asp Phe His Phe Glu Val Phe Asn Phe Val Pro Cys Ser Ile Cys Ser Asn

        550         559         568         577         586         595
    AAT CCA ACC ACC TGC TGG GCT ATC TGC AAA AGA ATA CCA AAC CCA GGA AAG
    Asn Pro Thr Cys Trp Ala Ile Cys Lys Arg Ile Pro Asn Lys Lys Pro Gly Lys

        604         613         622         631         640         649
    AAA ACC ACC ACC AAG CCT ACA AAA AAA CCA ACC TTC AAG ACA ACC AAA AAA GAT
    Lys Thr Thr Thr Lys Pro Thr Lys Lys Pro Thr Lys Pro Thr Phe Lys Thr Thr Lys Lys Asp
```

FIG.2C

```
      658         667         676         685         694         703
CTC AAA CCT CAA ACC ACT AAA CCA AAG GAA GTA CCC ACC AAG CCC ACA GAA
Leu Lys Pro Gln Thr Thr Lys Pro Lys Glu Val Pro Thr Lys Pro Thr Glu

      712         721         730         739         748         757
GAG CCA ACC ATC AAC ACC AAA ACC ACA AAC ATC ACA ACT ACA AAC CTG CTC ACC AAC
Glu Pro Thr Ile Asn Thr Lys Thr Thr Asn Ile Thr Thr Thr Asn Leu Leu Thr Asn

      766         775         784         793         802         811
AAC ACA GGA AAT CCA AAA CTC ACA AGT CAA ATG GAA ACC TTC CAC TCA ACC
Asn Thr Gly Asn Pro Lys Leu Thr Ser Gln Met Glu Thr Phe His Ser Thr

      820         829         838         847         856         865
TCC TCC GAA GGC AAT CTA AGC CCT TCT CAA GTC TCC ACA ACA TCC GAG CAC CCA
Ser Ser Glu Gly Asn Leu Ser Pro Ser Gln Val Ser Thr Thr Ser Glu His Pro

      874         883         892         901         914
TCA CAA CCC TCA TCT CCA CCC AAC ACA ACA CGC CAG TAGTTATTAA AAAAAAAA
Ser Gln Pro Ser Ser Pro Pro Asn Thr Thr Arg Gln            .
```

FIG.3A

```
CAC AAA GTC ACA CTA ACA ACT GCA ATC ATA CAA GAT GCA ACA AGC ATC AAG    54
His Lys Val Thr Leu Thr Thr Ala Ile Ile Gln Asp Ala Thr Ser Gln Ile Lys  18

AAC ACA ACC CCA ACA TAC CTC ACT CAG GAT CCT CAG CTT GGA ATC AGC TTC TCC  108
Asn Thr Thr Pro Thr Tyr Leu Thr Gln Asp Pro Gln Leu Gly Ile Ser Phe Ser  36

AAT CTG TCT GAA ATT ACA TCA CAA ACC ATA CTA GCT TCA ACA ACA CCA        162
Asn Leu Ser Glu Ile Thr Ser Gln Thr Ile Leu Ala Ser Thr Thr Pro         54

GGA GTC AAG TCA AAC CTG CAA CCC ACA GTC AAG ACT AAA AAC ACA ACA        216
Gly Val Lys Ser Asn Leu Gln Pro Thr Val Lys Thr Lys Asn Thr Thr          72

ACC CAA ACA CAA CCC AGC AAG CCC ACT ACA AAA CAA CGC CAA AAA CCA CCA    270
Thr Gln Thr Gln Pro Ser Lys Pro Thr Thr Lys Gln Arg Gln Asn Lys Pro Pro  90

AAC AAA CCC AAT AAT GAT TTT CAC TTC GAA GTG TTT AAC TTT GTA CCC TGC AGC  324
Asn Lys Pro Asn Asn Asp Phe His Phe Glu Val Phe Asn Phe Val Pro Cys Ser  108

ATA TGC AGC AAC AAT CCA ACC TGC TGG GCT ATC TGC AAA AGA ATA CCA AAC AAA  378
Ile Cys Ser Asn Asn Pro Thr Cys Trp Ala Ile Cys Lys Arg Ile Pro Asn Lys  126

AAA CCA GGA AAG AAA ACC ACC AAG CCT ACA AAA AAA CCA ACC TTC AAG ACA    432
Lys Pro Gly Lys Lys Thr Thr Lys Pro Thr Lys Lys Pro Thr Phe Lys Thr      144
```

FIG.3B

```
ACC AAA AAA GAT CTC AAA CCT CAA ACC ACT AAA CCA AAG GAA GTA CCC ACC ACC   486
Thr Lys Lys Asp Leu Lys Pro Gln Thr Thr Lys Pro Lys Glu Val Pro Thr Thr   162

AAG CCC ACA GAA GAG CCA ACC ATC AAC ACC AAA ACA AAC ATC ACA ACT ACA       540
Lys Pro Thr Glu Glu Pro Thr Ile Asn Thr Lys Thr Asn Ile Thr Thr Thr       180

CTG CTC ACC AAC ACC ACA GGA AAT CCA ACA AAA CTC ACA ATG GAA ACC           594
Leu Leu Thr Asn Asn Thr Gly Asn Pro Thr Lys Leu Thr Ser Gln Met Glu Thr   198

TTC CAC TCA ACC TCC TCC GAA GGC AAT CTA AGC CCT TCT CAA GTC TCC ACA ACA   648
Phe His Ser Thr Ser Ser Glu Gly Asn Leu Ser Pro Ser Gln Val Ser Thr Thr   216

TCC GAG CAC CCA TCA CAA CCC TCA TCT CCA CCC AAC ACA ACA CGC CAG TAG       699
Ser Glu His Pro Ser Gln Pro Ser Ser Pro Pro Asn Thr Thr Arg Gln     .      232

TTATTAA AAAAAAAA
```

Eco RI

Afl IIII

RSV G
pRSV G12
4130 bp

Eco RI

pCMV

VR 1012
4800 bp
Intron A

BGHpA

Eco RV

Afl III
Eco RI
Klenow

Eco RV

Ligate

pCMV

pXL5   Intron A
5820 bp

RSV G

BGHpA

FIG.4.

Eco RI
Bam HI

RSV G

pRSV G12
4130 bp

Eco RI

pCMV

Intron A

VR 1020
5100 bp

TPAsig

Bam HI

BGHpA

Bgl II

Eco RI
Klenow
Bam HI

Bgl II
Klenow
Bam HI

5' GATCCACTCAG 3' ——Ligate
    GTGAGTCCTAG

pCMV

pXL6
5734 bp   Intron A

TPA sig

RSV G

BGHpA

FIG.5

FIG.6A

```
          10         20         30         40         50         60         70
  TCGCGCGTTT CGGTGATGAC GGTGAAAAAC TCTGACACAT GCAGCTCCCG GAGACGGTCA CAGCTTGTCT

          80         90        100        110        120        130        140
  GTAAGCGGAT GCCGGGAGCA GACAAGCCCG TCAGGGGGTG TTGGGCGGTC TCGGGCCTG

         150        160        170        180        190        200        210
  CTTAACTATG CGGCATCAGA GCAGATTGTA CTGAGAGTGC ACCATATGCG GTGTGAAATA CCCGCACAGAT

         220        230        240        250        260        270        280
  GGGTAAGGAG AAAATACCGC ATCAGATTGG CTATTGGCCA TTGCATACGT TGTATCCATA TCATATAATG

         290        300        310        320        330        340        350
  TACATTTATA TTGCTTCATG TCCAACATTA CCGCCATGTT GACATTGATT ATTGACTAGT TATTAATAGT

         360        370        380        390        400        410        420
  AATCAATTAC GGGGTCATTA GTTCATAGCC CATATATGGA GTTCCCGCGTT ACATAACTTA CGGTAAATGG

         430        440        450        460        470        480        490
  CCCGCCTGGC TGACCGCCCA AGGACCCCCG CCCATTGACG TCAATAATGA CGTATGTTCC CATAGTAACG

         500        510        520        530        540        550        560
  CCAATAGGGA CTTTCCATTG ACGTCAATGG GTGGAGTATT TACGGTAAAC TGCCCACTTG GCAGTACATC
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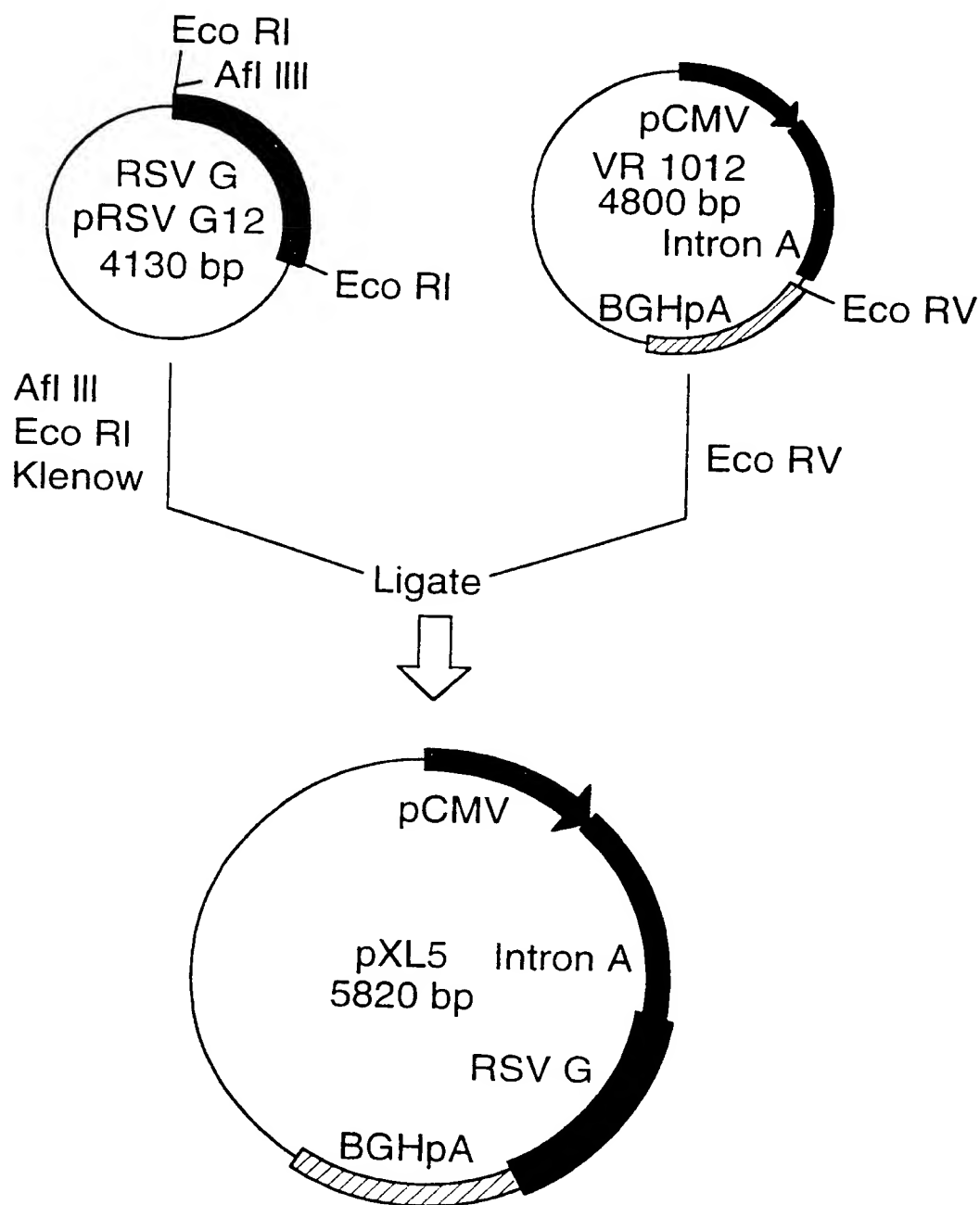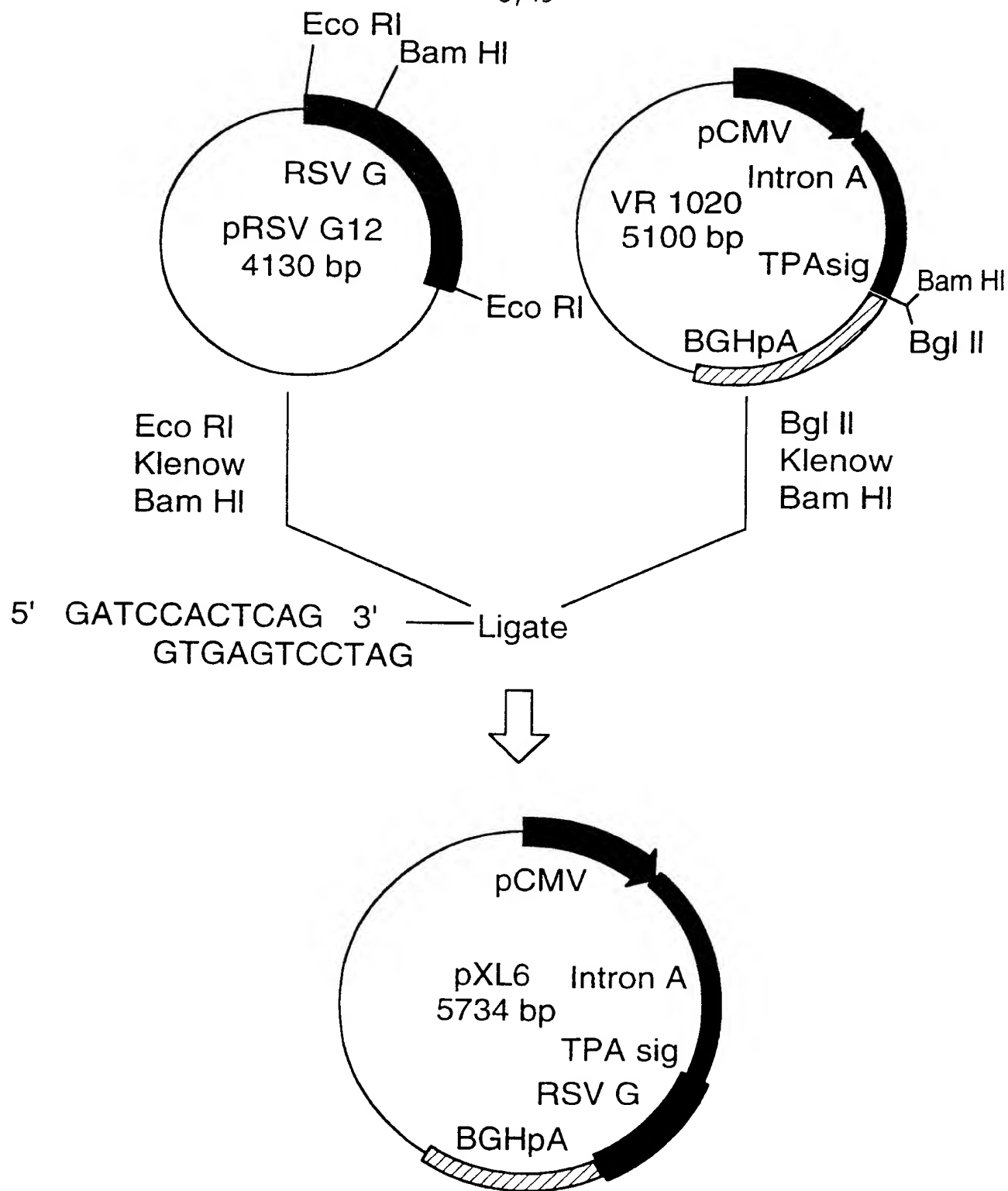
FIG.6B

```
        570        580        590        600        610        620        630
AAGTGTATCA TATGCCAAGT ACGCCCCCTA TTGCAGTCAA TGACGGTAAA TGGCCCGCCT GGCATTATGC

        640        650        660        670        680        690        700
CCAGTACATG ACCTTATTGG ACTTTCCTAC TTGGCAGTAC ATCTACGTAT TAGTCATCGC TATTACCATG

        710        720        730        740        750        760        770
GTGATGCGGT TTTGGCAGTA CATCAATGGG CGTGGATAGC GGTTTGACTC ACGGGGATTT CCAAGTCTCC

        780        790        800        810        820        830        840
ACCCCATTGA CGTCAATGGG AGTTTGTTTT GGCACCAAAA TCAACGGGAC TTTCCAAAAT GTCGTAACAA

        850        860        870        880        890        900        910
CTCCGCCCCA TTGACGCAAA TGGGCGGTAG GCGTGTACGG TGGGAGGTCT ATATAAGCAG AGCTGTTTA

        920        930        940        950        960        970        980
GTGAACCGTC AGATCGCCTG GAGACGCCAT CCACGCTGTT TTGACCTCCA TAGAAGACAC CGGGACCGAT

        990       1000       1010       1020       1030       1040       1050
CCAGCCTCCG CGGCCGGGAA CGGTGCATTG GAACGCGGAT TCCCCGTGCC AAGAGTGACG TAAGTACCGC

       1060       1070       1080       1090       1100       1110       1120
CTATAGACTC TATAGGCACA CCCCTTTGGC TCTTATGCAT GCTATACTGT TTTTGGCTTG GGGCCTATAC
```

FIG.6C

```
1130        1140        1150        1160        1170        1180        1190
ACCCCCGCTT  CCTTATGCTA  TAGGTGATGG  TATTAGCTTAG CCTATAGGTG  TGGGTTATTG  ACCATTATTG

1200        1210        1220        1230        1240        1250        1260
ACCACTCCCC  TATTGGTGAC  GATACTTTCC  ATTACTAAATC CATAACATGG  CTCTTTGCCA  CAACTATCTC

1270        1280        1290        1300        1310        1320        1330
TATTGGCTAT  ATGCCAATAC  TCTGTCCTTC  AGAGACTGAC  ACGGACTCTG  TATTTTTACA  GGATGGGGTC

1340        1350        1360        1370        1380        1390        1400
CCATTTATTA  TTTACAAATT  CACATATACA  ACAACGCCGT  CCCCGTGCC   CGCAGTTTTT  ATTAAACATA

1410        1420        1430        1440        1450        1460        1470
GGGTGGGATC  TCCACGGGAA  TCTCGGGTAC  GTGTTCCGGA  CATGGGCTCT  TCTCGGGTAG  CGGGGGAGCT

1480        1490        1500        1510        1520        1530        1540
TCCACATCCG  AGCCCTGGTC  CCATGCCTCC  AGGGGCTCAT  GGTCGCTCCG  CAGTCCTTG   CTCCTAACAG

1550        1560        1570        1580        1590        1600        1610
TGGAGGCCAG  ACTTAGGCAC  AGCACAATGC  CCACCACCAC  CAGTGTGCCG  CACAAGGCCG  TGGCGGTAGG

1620        1630        1640        1650        1660        1670        1680
GTATGTGTCT  GAAAAATGAGC GTGCAGATTG  GGCTCCGCACG GCTTGAGCGCAG ATGGAAGACT TAAGGCAGGG
```

FIG.6D

```
        1690       1700       1710       1720       1730       1740       1750
GCAGAAGAAG ATGCAGGCAG CTGAGTTGTT GTATTCTGAT AAGAGTCAGA GGTAACTCCC GTTGGGGTGC

        1760       1770       1780       1790       1800       1810       1820
TGTTAACGGT GGAGGGCAGT GTAGTCTGAG CAGTACTCGT TGCTGGGGG CGGGCCACCA GACATAATAG

        1830       1840       1850       1860       1870       1880       1890
CTGACAGACT AACAGACTGT TCCTTTCCAT GGGTCTTTTC TGCAGTCACC GTCGTCGACA CGTCGTGATCA

        1900       1910       1920       1930       1940       1950       1960
GATATCGGG CGGGCTCTAGA CCAGGGGCCT GGATCCAGAT CTGCTGTGCC TTCTAGTTGC CAGCCATCTG

        1970       1980       1990       2000       2010       2020       2030
TTGTTTGCCC CTCCCCCGTG CCTTCCTTGA CCCTGGAAG TGCCACTCCC ACTGTCCTTT CCTAATAAAA

        2040       2050       2060       2070       2080       2090       2100
TGAGGAAATT GCATCCCATT GTCTGAGTAG GTGTCATTCT ATTCTGGGG GTGGGGTGGG GCAGGACAGC

        2110       2120       2130       2140       2150       2160       2170
AAGGGGGAGG ATTGGGAAGA CAATAGCAGG CATGCTGGG ATGGGGTGGG CTCTATGGT ACCCAGGTGC

        2180       2190       2200       2210       2220       2230       2240
TGAAGAATTG ACCCGGTTCC TCCTGGGCCA GAAAGAAGCA GGCACATCCC CTTCTCTGTG ACACACCCTG
```

FIG.6E

```
        2250       2260       2270       2280       2290       2300       2310
   TCCAGCCCC  TGGTTCTTAG  TTCCAGCCCC  ACTCATAGGA  CACTTCATAGC  TCAGGAGGC  TCGGCCTTCA

        2320       2330       2340       2350       2360       2370       2380
   ATCCCACCCG  CTAAAGTACT  TGGAGCGGTC  TCTCCCTCCC  TCATCAGCCC  ACCAAACCAA  ACCTAGCCTC

        2390       2400       2410       2420       2430       2440       2450
   CAAGAGTGGG  AAGAAATTAA  AGCAAGATAG  GCTATTAAGT  GCAGAGGGAG  AGAAAATCCC  TCCAACATGT

        2460       2470       2480       2490       2500       2510       2520
   GAGGAAGTAA  TGAGAGAAAT  CATAGAATTT  CTTCCGCTTC  CTCGCTCACT  GACTCGGTGC  GCTCGGTTGT

        2530       2540       2550       2560       2570       2580       2590
   TCGGCTGCGG  CGAGCGGTAT  CAGCTCACTC  AAAGGCGGTA  ATACGGTTAT  CCACAGAATC  AGGGGATAAC

        2600       2610       2620       2630       2640       2650       2660
   GCAGGAAAGA  ACATGTGAGC  AAAAGGCCAG  CAAAAGGCCA  GGAACCGTAA  AAAGGCCGCG  TTGCTGGCGT

        2670       2680       2690       2700       2710       2720       2730
   TTTTCCATAG  GCTCCGCCCC  CCTGACGAGC  ATCACAAAAA  TCGACGCTCA  AGTCAGAGGT  GGCGAAACCC

        2740       2750       2760       2770       2780       2790       2800
   GACAGGACTA  TAAAGATACC  AGGCGTTTCC  CCCTGGAAGC  TCCCTCGTGC  GCTCTCCTGT  TCCGACCCTG
```

FIG.6F

```
       2810       2820       2830       2840       2850       2860       2870
  CCGCTTACCG GATACCTGTC CGCCTTTCTC CCTTCGGGAA GCGTGGCGCT TTCTCATAGC TCACGCTGTA

       2880       2890       2900       2910       2920       2930       2940
  GGTATCTCAG TTCGGTGTAG GTCGTTCGCT CCAAGCTGGG CTGTGTGCAC GAACCCCCCG TTCAGCCCGA

       2950       2960       2970       2980       2990       3000       3010
  CCGCTGCGCC TTATCCGGTA ACTATCGTCT TGAGTCCAAC CCGGTAAGAC ACGACTTATC GCCACTGGCA

       3020       3030       3040       3050       3060       3070       3080
  GCAGCCACTG GTAACAGGAT TAGCAGAGCG AGGTATGTAG GCGGTGCTAC AGAGTTCTTG AAGTGGTGGC

       3090       3100       3110       3120       3130       3140       3150
  CTAACTACGG CTACACTAGA AGAACAGTAT TTGGTATCTG CGCTCTGCTG AAGCCAGTTA CCTTCGGAAA

       3160       3170       3180       3190       3200       3210       3220
  AAGAGTTGGT AGCTCTTGAT CCGGCAAACA AACCACCGCT GGTAGCGGTG GTTTTTTTGT TTGCAAGCAG

       3230       3240       3250       3260       3270       3280       3290
  CAGATTACGC GCAGAAAAAA AGGATCTCAA GAAGATCCTT TGATCTTTTC TACGGGGTCT GACGCTCAGT

       3300       3310       3320       3330       3340       3350       3360
  GGAACGAAAA CTGACGTTAA GGGATTTTGG TCATGAGATT ATCAAAAAGG ATCTTCACCT AGATCCTTTT
```

FIG.6G

G

WO 99/04010 PCT/CA98/00697

15/19

```
3370       3380       3390       3400       3410       3420       3430
AAATTAAAAA TGAAGTTTTA AATCAATCTA AAGTATATAT GAGTAAACTT GGTCTGACAG TTACCAATGC

3440       3450       3460       3470       3480       3490       3500
TTAATCAGTG AGGCACCTAT CTCAGGGATC TGTCTATTTC GTTCATCAT  AGTTGCCTGA CTCGGGGGGG

3510       3520       3530       3540       3550       3560       3570
GGGGGCTG   AGGTCTGCCT CGTGAGAGAAG GTGTTGCTGA CTCATACCAG GCCTGAATCG CCCCATCATC

3580       3590       3600       3610       3620       3630       3640
CAGCCAGAAA GTGAGGGAGC CACGGTTGAT GAGAGCTTTG TTGTAGGTGG ACCAGTTGT  GATTTTGAAC

3650       3660       3670       3680       3690       3700       3710
TTTTGCTTTG CCACGGAAGC GTCTGGGTTG TCGGGAAGAT GGGTGATCTG ATCCTTCAAC TCAGCAAAG

3720       3730       3740       3750       3760       3770       3780
TTCGATTTAT TCAACAAAGC CCCGTCCCG  TCAAGTCAGC GTAATCCTCT GCCAGTGTTA CAACCAATTA

3790       3800       3810       3820       3830       3840       3850
ACCAATTGTG ATTAGAAAAA CTCATCGAGC ATCAAATGAA ACTGCCAATTT ATTCATATCA GGATTATCAA

3860       3870       3880       3890       3900       3910       3920
TACCATATTT TTGAAAAAGC CGTTTCTGTA ATGAAGGAGA AAACTCACCG AGGCAGTTCC ATAGGATGGC
```

FIG.6H

```
        3930       3940       3950       3960       3970       3980       3990
AATATCCTTG TATCGGTCTG CGATTCCGAC TGTCCAACA TCAATACAAC CTATTAATTT CCCTTGTCA

        4000       4010       4020       4030       4040       4050       4060
AAAATAAGGT TATCAAGTGA GAAATCACCA TGAGTGACGA CTGAATCCGG TGAGAATGGC AAAAGCTTAT

        4070       4080       4090       4100       4110       4120       4130
GCATTCTTT CCAGACTTGT TCAACAGGCC AGCCATTACG CTGTCATCA AAATCACTCG CATCAACCAA

        4140       4150       4160       4170       4180       4190       4200
ACGGTTATTC ATTCGTGATT GGGCCTGAGC GAGACGAAAT ACGGATGGC TGTTAAAAG ACAATTACAA

        4210       4220       4230       4240       4250       4260       4270
ACAGGAATCG AATGCAACCG GGGCAGAAC ACTGCCAGCG CATCAACAAT ATTTTCACCT GAATCAGGAT

        4280       4290       4300       4310       4320       4330       4340
ATTCTTCTAA TACCTGGAAT GCTGTTTCC CGGGATCGC AGTGGTGAGT AACCATGCAT CATCAGGAGT

        4350       4360       4370       4380       4390       4400       4410
ACGGATAAAA TGCTTGATGG TCGGAAGAGG CATAAATTCC GTCAGCCAGT TTAGTCTGAC CATTCATCT

        4420       4430       4440       4450       4460       4470       4480
GTAACATCAT TGGCAACGCT ACCTTTGCCA TGTTTCAGAA ACAACTCTGG CGCATCGGGC TTCCCATACA
```

FIG.6I

```
4490       4500       4510       4520       4530       4540       4550
ATGGATAGAT TGTGGCACCT GATTGCCGGA CATTATGCGG AGCCCATTTA TACCCATATA AATCAGCATC

4560       4570       4580       4590       4600       4610       4620
CATGTTGGAA TTTAATGGCG GCCTTGGAGCA AGAGCGTTTCC CGTTGAATAT GCCTCATAAC GTTCCTTGTA

4630       4640       4650       4660       4670       4680       4690
TTTACTGTTTA TGTAAGCAGA CAGTTTATT GTTCATGATG ATATATTTTT ATCTTGTGCA ATGTAACATC

4700       4710       4720       4730       4740       4750       4760
AGAGATTTTG AGACACAACG TGGCTTTCCC CCCCCCCCA TTATTGAAGC ATTTATCAGG GTTATTGTCT

4770       4780       4790       4800       4810       4820       4830
CATGAGCGGA TACATATTTG AATGTATTTA GAAAAATAAA CAAATAGGGG TTCGGGCGAC ATTTCCCGA

4840       4850       4860       4870       4880       4890       4900
AAAGTGCCAC CTGAGCTCTA AGAAACCATT ATTTATCATGA CATTAACCTA TAAAAATAGG CGTATCACGA

4910
GGCCCTTTCG TC
```

FIG.7

```
         10          20          30          40          50          60          70
CTGCAGTCAC  CGTCGTTGAC  CAGAGCTTGAG  ATCCTACAGG  AGTCCAGGC  TGGAGAGAAA  ACCTCTGGGA

         80          90          100         110         120         130         140
GGAAAGGGAA  GGAGCAAGCC  GTGAATTTAA  GGGACGCTGT  GAAGCAATCA  TGGATGCAAT  GAAGAGAGG

        150         160         170         180
CTCTCGCTGTG  TGCTCGCTGCT  GTGTCGGAGCA  GTCTTCGTTT  CGCCCCAGC
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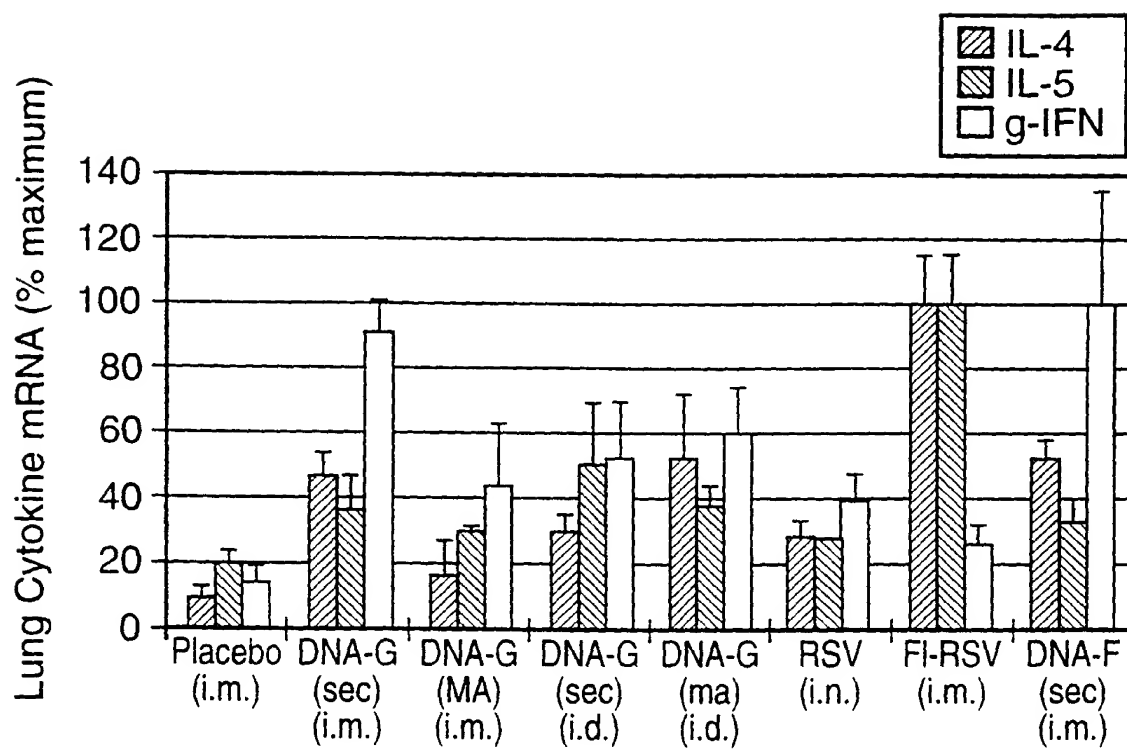
FIG.8